OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/032,106

DATE: 04/25/2002
TIME: 15:14:47

Input Set : A:\43311-20007.00.txt
Output Set: N:\CRF3\04252002\J032106.raw

ENTERED

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      4 <110> APPLICANT: Peng, Zaoyuan
      5       Yu, Zailin
      6       Wiley, Andrew
      7       Hu, Qianjin
      9 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING G-PROTEIN
     10       COUPLED RECEPTORS ASSOCIATED WITH DISEASES
     13 <130> FILE REFERENCE: 433112000700
     15 <140> CURRENT APPLICATION NUMBER: US 10/032,106
C--> 16 <141> CURRENT FILING DATE: 2002-04-08
     18 <150> PRIOR APPLICATION NUMBER: US 60/258,070
     19 <151> PRIOR FILING DATE: 2000-12-20
     21 <160> NUMBER OF SEQ ID NOS: 10
     23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     26 <211> LENGTH: 924
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Homo sapiens
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     32 tggcaagttc tcttcttcat catctttctt gtggtctaca tcatcaccat ggtgggcaat     120
     33 atcggcatga tggtgttaat caaggtcagt cctcagctta acaaccccat gtacttttc     180
     34 ctcagtcact tgtcatttgt tgatgtgtgg ttttcttcca atgtcacccc taaaatgttg     240
     35 gaaaacctgt tttcagataa aaaaacaatt acttatgctg gttgtttagt acagtgtttc     300
     36 ttcttcattg ctcttgtcca tgtggaaatt tttattcttg ctgcgatggc ctttgataga     360
     37 tacatggcaa ttgggaatcc tctgctttat ggcagtaaaa tgtcaagggt tgtctgtatt     420
     38 cgactgatta ctttccctta catttatggt tttctgacga gtctggcagc aacattatgg     480
     39 acttacggct tgtacttctg tggaaaaatt gagatcaacc atttctactg tgcagatcca     540
     40 cctctcatca aaatggcctg tgccgggacc tttgtaaaag aatatacaat gatcatactt     600
     41 gccggcatta acttcacata ttccctgact gtaattatca tctcttactt attcatcctc     660
     42 attgccattc tgcgaatgcg ctcagcagaa ggaaggcaga aggccttttc cacatgtggg     720
     43 tcccatctga cagctgtcat tatattctat ggtactctga tcttcatgta tctcagacgt     780
     44 cccacagagg agtctgtgga gcaggggaag atggtggctg tgttctatac cacagtgatc     840
     45 cccatgttga atcccatgat ctacagtctg aggaacaagg atgtgaaaaa ggccatgatg     900
     46 aaagtgatca gcagatcatg ttaa                                           924
     48 <210> SEQ ID NO: 2
     49 <211> LENGTH: 939
     50 <212> TYPE: DNA
     51 <213> ORGANISM: Homo sapiens
     53 <400> SEQUENCE: 2
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     55 cctcagctgg agctagtcct ctttgtggtt cttttgatct tctatatctt cactttgctg     120
     56 gggaacaaaa ccatcattgt attatctcac ttggacccac atcttcacac tcctatgtat     180
     57 tttttcttct ccaacctaag ctttttggat ctgtgttaca caaccggcat tgttccacag     240
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ctcctggtta atctcagggg agcagacaaa tcaatctcct atggtggttg tgtagttcag 300
ctgtacatct ctctaggctt gggatctaca gaatgcgttc tcttaggagt gatggtattt 360
gaccgctatg cagctgtttg caggcccctc cactacacag tagtcatgca cccttgtctg 420
tatgtgctga tggcttctac ttcatgggtc attggttttg ccaactccct attgcagacg 480
gtgctcatct tgcttttaac actttgtgga agaaataaat tagaacactt tctttgtgag 540
gttcctccat tgctcaagct tgcctgtgtt gacactacta tgaatgaatc tgaactcttc 600
tttgtcagtg tcattattct tcttgtacct gttgcattaa tcatattctc ctatagtcag 660
attgtcaggg cagtcatgag gataaagtta gcaacagggc agagaaaagt gtttgggaca 720
tgtggctccc acctcacagt ggtttccctg ttctacggca cagctatcta tgcttacctc 780
cagcccggca acaactactc tcaggatcag ggcaagttca tctctctctt ctacaccatc 840
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cttaagaagg tgctctggaa gaactacgac tccagatga 939

<210> SEQ ID NO: 3
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(930)
<223> OTHER INFORMATION: n= a, c, g, or t

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gggaacctgg gcatgatcac tctaatttgt ctgaactctc agctgcacac ccccatgtac 180
tactttctca gcaatctgtc actcatggat ctctgctact cctccgtcat taccctaag 240
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ctctacttct tccttgtttt tgtcattgct gagtgttaca tgctgacagt gatggcctac 360
W--> **gaccgctatg ttgncntctg ccacccttg ctttacaaca tcattatgtc tcatcacacc 420**
tgcctgctgc tggtggctgt ggtctacgcc atcggactca ttggctccac aatagaaact 480
ggcctcatgt taaaactgcc ctattgtgag cacctcatca gtcactactt ctgtgacatc 540
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ccctccacaa tcagttcctt gacccaggag aatgtggcct ctgtgttcta caccacggta 840
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cagaaaacgc tgaggggtaa actgttttga 930

<210> SEQ ID NO: 4
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 4
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cctcaatgga gagacacgtt tttcacatta gtgctgataa tttacctcag cacattgttg 120
gggaatggat ttatgatctt tcttattcac tttgacccca acctccacac tccaatctac 180
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gctttggtgc attgtttctc tacccatccc tacctctctt atccccgatg tttggctcaa 300
acgagtgtct ccttggcttt ggccacagca gagtgcctcc tactggctgc catggcctat 360
gaccgtgtgg ttgctatcag caatcccctg cgttattcag tggttatgaa tggcccagta 420

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tgtgtctgct tggttgctac ctcatggggg acatcacttg tgctcactgc catgctcatc 480
ctatccctga ggcttcactt ctgtggggct aatgtcatca accattttgc ctgtgagatt 540
ctctccctca ttaagctgac ctgttctgat accagcctca atgaatttat gatcctcatc 600
accagtatct tcaccctgct gctaccattt gggtttgttc tcctctccta catacgaatt 660
gctatggcta tcataaggat tcgctcactc cagggcaggc tcaaggcctt taccacatgt 720
ggctctcacc tgaccgtggt gacaatcttc tatgggtcag ccatctccat gtatatgaaa 780
actcagtcca agtcctaccc tgaccaggac aagtttatct cagtgtttta tggagctttg 840
acacccatgt tgaacccccc gatatatagc ctgagaaaaa aagatgttaa acgggcaata 900
aggaaagtta tgttgaaaag gacatga 927

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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ctgcttggaa actgcactct ccttctcatc atccaggctg atgcagccct ccatgaaccc 180
atgtacctct ttctggccat gttggcagcc atcgacctgg tcctttcctc ctcagcactg 240
cccaaaatgc ttgccatatt ctggttcagg gatcgggaga taaacttctt tgcctgtctg 300
gcccagatgt tcttccttca ctccttctcc atcatggagt cagcagtgct gctggccatg 360
gcctttgacc gctatgtggc tatctgcaag ccactgcact acaccaaggt cctgactggg 420
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tgtgaacaca tggctgtggt gaggctggcg tgtggggaca ctagcttcaa caatatctat 600
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tcagtcatgc accgtgtagc ccgccatgct gcccctcatg tccacatcct ccttgccaat 840
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atccgtgaga gcatcttggg agtattccca agaaaggata tgtag 945

<210> SEQ ID NO: 6
<211> LENGTH: 307
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6
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20 25 30
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys
35 40 45
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu
50 55 60
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu
65 70 75 80
Glu Asn Leu Phe Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu
85 90 95
Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile
100 105 110

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165 Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu
166         115                 120                 125
167 Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr
168     130                 135                 140
169 Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp
170 145                 150                 155                 160
171 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr
172                 165                 170                 175
173 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val
174             180                 185                 190
175 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser
176         195                 200                 205
177 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu
178     210                 215                 220
179 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly
180 225                 230                 235                 240
181 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met
182                 245                 250                 255
183 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
184             260                 265                 270
185 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
186         275                 280                 285
187 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser
188     290                 295                 300
189 Arg Ser Cys
190 305
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193 <211> LENGTH: 312
194 <212> TYPE: PRT
195 <213> ORGANISM: Homo sapiens
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200 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu
201             20                  25                  30
202 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
203         35                  40                  45
204 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser
205     50                  55                  60
206 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
207 65                  70                  75                  80
208 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
209                 85                  90                  95
210 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys
211             100                 105                 110
212 Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg
213         115                 120                 125
214 Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
215     130                 135                 140
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216 Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
217 145                 150                 155                 160
218 Val Leu Ile Leu Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
219                 165                 170                 175
220 Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
221             180                 185                 190
222 Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
223         195                 200                 205
224 Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
225     210                 215                 220
226 Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
227 225                 230                 235                 240
228 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
229                 245                 250                 255
230 Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
231             260                 265                 270
232 Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
233         275                 280                 285
234 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
235     290                 295                 300
236 Leu Trp Lys Asn Tyr Asp Ser Arg
237 305                 310
239 <210> SEQ ID NO: 8
240 <211> LENGTH: 309
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: VARIANT
246 <222> LOCATION: (1)...(309)
247 <223> OTHER INFORMATION: Xaa= any amino acid
249 <400> SEQUENCE: 8
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253             20                  25                  30
254 Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
255         35                  40                  45
256 Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
257     50                  55                  60
258 Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
259 65                  70                  75                  80
260 Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
261                 85                  90                  95
262 Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
263             100                 105                 110
W--> 264 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Xaa Xaa Cys His
265         115                 120                 125
266 Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
267     130                 135                 140
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 374,376
Seq#:8; Xaa Pos. 125,126